Model Cultures versus Field Molecular Tools: Are the Cells We Use in the Lab the Cells We "See" in the Field

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Background. Model cultures (pure or mixed cultures) are often used in environmental remediation research to quantify rates and extent of biotransformation. While this is practically simpler than using environmental samples, there may be a disconnect between the cells selected for laboratory studies and the cells identified in the field. However, when the same cells have been used in lab studies as those found in the field, then lab derived rates and mechanisms are useful for predicting field biodegradation dynamics. One key to this type of comparison is the appropriate use of molecular biology tools (on field and lab samples), so the data, phyla, and functional genes can be compared amongst the treatments and strategies involved. The objective of this presentation is to review a number of lab and field applications of molecular biology tools and model culture experiments, to identify situations in which it may have been more or less appropriate to use lab data as a predictive tool for field applications. One specific sub topic will be identifying low cell-density number, unique phyla that may be critical to biodegradation, but for which there are no reasonable model cultures to use in lab studies.

Approach. The results will be a combination of both lab and field molecular biology data related to three primary contaminants: trichloroethylene (TCE), explosives (RDX), and fuel oxygenates (tert butyl alcohol). In each case presented there were corollary lab and field studies running concurrently, and molecular biology tools such as quantitative PCR, high throughout sequencing of 16S rRNA gene (Illumina MiSeq), and standard molecular tools including cloning were used. In addition, "model" cultures (pure and mixed) were selected a priori based on the literature prior to these studies, and several model cultures were used to predict what may happen in the field incubations and field applications.

Results. Data demonstrate that the specific contaminant dictated which of the molecular biology tools in the lab versus field, and which model cultures were most appropriate for making comparisons between lab data and field applications. Chlorinated solvent data, not surprisingly, were relatively consistent between the lab and field. This is due to the fact that complete reductive dechlorination has thus far been catalyzed by a single phylum – *Dehalococcoides* spp., and as such the data generated in the lab with model DHC like cells carries well to the field. However, the rate and extent of dechlorination was different when using model bioaugmentation cultures and field material. Explosives such as RDX fell into a middle ground, in which some model culture data compared favorably with field data, and in other cases the model cultures used were not identified in any field samples. These data suggest that perhaps field sampling and analyses should precede lab studies in all cases, to select the "best" model cultures. Finally, tert-butyl alcohol biodegradation screening at multiple field sites across the United States indicated that biodegradation did not correlate with any model organisms reported in the literature. In fact, molecular biology tools indicated that TBA was biodegraded by unique phyla that were a very limited proportion of the total microbial community. This suggests that TBA biodegradation applications benefit greatly from field molecular biology tools, because often the same unique phyla were identified in disparate sites. These unique phyla have no model culture representation for lab studies.